PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION . US/08/423,194A

1812

DATE: 02/23/97
TIME: 07:42:39

INPUT SET: S15803.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                                    SEQUENCE LISTING  ENTERED
 2
 3  (1)     General Information:
 4
 5     (i) APPLICANT: Eaton, Dan L.
 6                    de Sauvage, Frederic J.
 7
 8    (ii) TITLE OF INVENTION: MPL LIGAND
 9
10   (iii) NUMBER OF SEQUENCES: 77
11
12    (iv) CORRESPONDENCE ADDRESS:
13         (A) ADDRESSEE: Genentech, Inc.
14         (B) STREET: 460 Point San Bruno Blvd
15         (C) CITY: South San Francisco
16         (D) STATE: California
17         (E) COUNTRY: USA
18         (F) ZIP: 94080
19
20     (v) COMPUTER READABLE FORM:
21         (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22         (B) COMPUTER: IBM PC compatible
23         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24         (D) SOFTWARE: WinPatin (Genentech)
25
26    (vi) CURRENT APPLICATION DATA:
27         (A) APPLICATION NUMBER: 08/423194
28         (B) FILING DATE: 18-Apr-1995
29         (C) CLASSIFICATION:
30
31   (vii) PRIOR APPLICATION DATA:
32         (A) APPLICATION NUMBER: 08/249376
33         (B) FILING DATE: 25-MAY-1994
34
35   (vii) PRIOR APPLICATION DATA:
36         (A) APPLICATION NUMBER: 08/223263
37         (B) FILING DATE: 04-APR-1994
38
39   (vii) PRIOR APPLICATION DATA:
40         (A) APPLICATION NUMBER: 08/196689
41         (B) FILING DATE: 15-FEB-1994
42
43   (vii) PRIOR APPLICATION DATA:
44         (A) APPLICATION NUMBER: 08/185607
45         (B) FILING DATE: 21-JAN-1994
46
```

```
47   (vii) PRIOR APPLICATION DATA:
48         (A) APPLICATION NUMBER: 08/176553
49         (B) FILING DATE: 03-JAN-1994
50
51   (viii) ATTORNEY/AGENT INFORMATION:
52         (A) NAME: Winter, Daryl B.
53         (B) REGISTRATION NUMBER: 32,637
54         (C) REFERENCE/DOCKET NUMBER: P0871P4D2
55.
56    (ix) TELECOMMUNICATION INFORMATION:
57         (A) TELEPHONE: 415/225-1249
58         (B) TELEFAX: 415/952-9881
59         (C) TELEX: 910/371-7168
60
61   (2) INFORMATION FOR SEQ ID NO:1:
62
63     (i) SEQUENCE CHARACTERISTICS:
64         (A) LENGTH: 353 amino acids
65         (B) TYPE: Amino Acid
66         (D) TOPOLOGY: Linear
67
68    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70   Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
71   -21 -20             -15             -10
72
73   Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
74        -5              1               5
75
76   Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
77    10              15              20
78
79   Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
80    25              30              35
81
82   Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
83    40              45              50
84
85   Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
86    55              60              65
87
88   Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
89    70              75              80
90
91   Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
92    85              90              95
93
94   Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
95    100             105             110
96
97   Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
98    115             120             125
99
```

INPUT SET: S15803.raw

```
100    Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
101    130             135             140
102
103    Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
104    145             150             155
105
106    Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu
107    160             165             170
108
109    Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser
110    175             180             185
111
112    Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe
113    190             195             200
114
115    Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu
116    205             210             215
117
118    Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn
119    220             225             230
120
121    Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly
122    235             240             245
123
124    Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro
125    250             255             260
126
127    Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro
128    265             270             275
129
130    Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr
131    280             285             290
132
133    Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro
134    295             300             305
135
136    Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His
137    310             315             320
138
139    Ser Gln Asn Leu Ser Gln Glu Gly
140    325             330     332
141
142    (2) INFORMATION FOR SEQ ID NO:2:
143
144       (i) SEQUENCE CHARACTERISTICS:
145          (A) LENGTH: 1795 base pairs
146          (B) TYPE: Nucleic Acid
147          (C) STRANDEDNESS: Single
148          (D) TOPOLOGY: Linear
149
150      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
151
152
```

INPUT SET: S15803.raw

```
153   TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50
154
155   CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCTTGG CCCGCCTTTG 100
156
157   CCCCACCCTA CTCTGCCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
158
159   CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
160
161   GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
162
163   TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
164
165   ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
166
167   AGACTGAGCC AGTGCCCAGA GGTTCACCCT TTGCCTACAC CTGTCCTGCT 400
168
169   GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
170
171   CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
172
173   ATGGCAGCAC GGGGACAACT GGGACCCACT TGCCTCTCAT CCCTCCTGGG 550
174
175   GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
176
177   TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
178
179   AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCGTTT 700
180
181   CCTGATGCTT GTAGGAGGGT CCACCCTCTG CGTCAGGCGG GCCCCACCCA 750
182
183   CCACAGCTGT CCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
184
185   CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
186
187   AACTACTGGC TCTGGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
188
189   TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
190
191   TACCTGAACA GGATACACGA ACTCTTGAAT GGAACTCGTG GACTCTTTCC 1000
192
193   TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTTCC TCAGGAACAT 1050
194
195   CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100
196
197   CCAACCCATC CTCCTACTGG ACAGTATACG CTCTTCCCTC TTCCACCCAC 1150
198
199   CTTGCCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTTCTG 1200
200
201   CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
202
203   TCCCAGAATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
204
205   AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350
```

```
206
207   AACTGGACAA GATTTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
208
209   GGGATACACA GGACTGAAAA GGGAATCATT TTTCACTGTA CATTATAAAC 1450
210
211   CTTCAGAAGC TATTTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
212
213   GCTCTTTGGT CTATTTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550
214
215   TGCTCTTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
216
217   GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
218
219   TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCATCC CCTTTACTAT 1700
220
221   CATTCTCAGT GGGACTCTGA TCCCATATTC TTAACAGATC TTTACTCTTG 1750
222
223   AGAAATGAAT AAGCTTTCTC TCAGAAAAAA AAAAAAAAAA AAAAA 1795
224
225   (2) INFORMATION FOR SEQ ID NO:3:
226
227      (i) SEQUENCE CHARACTERISTICS:
228          (A) LENGTH: 42 amino acids
229          (B) TYPE: Amino Acid
230          (D) TOPOLOGY: Linear
231
232      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
233
234   Leu Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu
235   -16 -15                -10                      -5
236
237   Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys
238        1              5                  10
239
240   Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu
241    15               20                  25  26
242
243   (2) INFORMATION FOR SEQ ID NO:4:
244
245      (i) SEQUENCE CHARACTERISTICS:
246          (A) LENGTH: 390 base pairs
247          (B) TYPE: Nucleic Acid
248          (C) STRANDEDNESS: Single
249          (D) TOPOLOGY: Linear
250
251      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
252
253
254   GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT 50
255
256   CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT 100
257
258   GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT 150
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/423,194A*

DATE: 02/28/97
TIME: 07:42:57

INPUT SET: S15803.raw

Line	Error	Original Text
27	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/423194